3119

OIPE

ENTERED

RAW SEQUENCE LISTING   DATE: 03/06/2002
PATENT APPLICATION: US/09/986,224   TIME: 12:40:28

Input Set : A:\07334-333001.txt
Output Set: N:\CRF3\03062002\I986224.raw

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     4 <110> APPLICANT: Bertin, John
     5        Wang,Weiye
     6        Blatcher, Maria
     8 <120> TITLE OF INVENTION: NOVEL MOLECULES OF THE NBS/LRR PROTEIN FAMILY AND USES
THEREOF
    10 <130> FILE REFERENCE: 07334-333001
    12 <140> CURRENT APPLICATION NUMBER: US 09/986,224
W--> 13 2001-10-22
C--> 15 <141> CURRENT FILING DATE: 2001-10-22
    15 <150> PRIOR APPLICATION NUMBER: US 09/848,035
    16 <151> PRIOR FILING DATE: 2001-05-03
    18 <150> PRIOR APPLICATION NUMBER: US 60/201,464
    19 <151> PRIOR FILING DATE: 2000-05-03
    21 <160> NUMBER OF SEQ ID NOS: 20
    23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    25 <210> SEQ ID NO: 1
    26 <211> LENGTH: 2464
    27 <212> TYPE: DNA
    28 <213> ORGANISM: Homo sapiens
    30 <220> FEATURE:
    31 <221> NAME/KEY: CDS
    32 <222> LOCATION: (1)...(2463)
    34 <400> SEQUENCE: 1
    35 atg aca tcg ccc cag cta gag tgg act ctg cag acc ctt ctg gag cag      48
    36 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln
    37  1               5                  10                  15
    39 ctg aac gag gat gaa tta aag agt ttc aaa tcc ctt tta tgg gct ttt      96
    40 Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe
    41             20                  25                  30
    43 ccc ctc gaa gac gtg cta cag aag acc cca tgg tct gag gtg gaa gag     144
    44 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu
    45             35                  40                  45
    47 gct gat ggc aag aaa ctg gca gaa att ctg gtc aac acc tcc tca gaa     192
    48 Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu
    49         50                  55                  60
    51 aat tgg ata agg aat gcg act gtg aac atc ttg gaa gag atg aat ctc     240
    52 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu
    53  65                  70                  75                  80
    55 acg gaa ttg tgt aag atg gca aag gct gag atg atg gag gac gga cag     288
    56 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln
    57                 85                  90                  95
    59 gtg caa gaa ata gat aat cct gag ctg gga gat gca gaa gaa gac tcg     336
    60 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser
    61                 100                 105                 110
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63 gag tta gca aag cca ggt gaa aag gaa gga tgg aga aat tca atg gag      384
64 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu
65         115                 120                 125
67 aaa caa tct ttg gtc tgg aag aac acc ttt tgg caa gga gac att gac      432
68 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp
69     130                 135                 140
71 aat ttc cat gac gac gtc act ctg aga aac caa cgg ttc att cca ttc      480
72 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe
73 145                 150                 155                 160
75 ttg aat ccc aga aca ccc agg aag cta aca cct tac acg gtg gtg ctg      528
76 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu
77                 165                 170                 175
79 cac ggc ccc gca ggc gtg ggg aaa acc acg ctg gcc aaa aag tgt atg      576
80 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met
81                 180                 185                 190
83 ctg gac tgg aca gac tgc aac ctc agc ccg acg ctc aga tac gcg ttc      624
84 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe
85         195                 200                 205
87 tac ctc agc tgc aag gag ctc agc cgc atg ggc ccc tgc agt ttt gca      672
88 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala
89     210                 215                 220
91 gag ctg atc tcc aaa gac tgg cct gaa ttg cag gat gac att cca agc      720
92 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser
93 225                 230                 235                 240
95 atc cta gcc caa gca cag aga atc ctg ttc gtg gtc gat ggc ctt gat      768
96 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp
97                 245                 250                 255
99 gag ctg aaa gtc cca cct ggg gcg ctg atc cag gac atc tgc ggg gac      816
100 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp
101                 260                 265                 270
103 tgg gag aag aag aag ccg gtg ccc gtc ctc ctg ggg agt ttg ctg aag     864
104 Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys
105                 275                 280                 285
107 agg aag atg tta ccc agg gca gcc ttg ctg gtc acc acg cgg ccc agg     912
108 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg
109     290                 295                 300
111 gca ctg agg gac ctc cag ctc ctg gcg cag cag ccg atc tac ata agg     960
112 Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg
113 305                 310                 315                 320
115 gtg gag ggc ttc ctg gag gag gac agg agg gcc tat ttc ctg aga cac     1008
116 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His
117                 325                 330                 335
119 ttt gga gac gag gac caa gcc atg cgt gcc ttt gag cta atg agg agc     1056
120 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser
121                 340                 345                 350
123 aac gcg gcc ctg ttc cag ctg ggc tcg gcc ccc gcg gtg tgc tgg att     1104
124 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile
125                 355                 360                 365
127 gtg tgc acg act ctg aag ctg cag atg gag aag ggg gag gac ccg ccg     1152
```

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128 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro
129     370             375             380
131 gtt ccc gca ggg cgc aca gct gcg ggg cgc gct gcg gac gct gag cct    1200
132 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro
133 385             390             395             400
135 cct ggc cgc gca ggg ctg tgg gcg cag atg tcc gtg ttc cac cga gag    1248
136 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu
137             405             410             415
139 gac ctg gaa agg ctc ggg gtg cag gag tcc gac ctc cgt ctg ttc ctg    1296
140 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
141             420             425             430
143 gac gga gac atc ctc cgc cag gac aga gtc tcc aaa ggc tgc tac tcc    1344
144 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
145         435             440             445
147 ttc atc cac ctc agc ttc cag cag ttt ctc act gcc ctg ttc tac gcc    1392
148 Phe Ile His Leu Ser Phe Gln Gln Phe Leu Thr Ala Leu Phe Tyr Ala
149     450             455             460
151 ctg gag aag gag gag gag gag gac agg gac ggc cac gcc tgg gac att    1440
152 Leu Glu Lys Glu Glu Glu Glu Asp Arg Asp Gly His Ala Trp Asp Ile
153 465             470             475             480
155 ggg gac gta cag aag ctg ctt tcc gga gaa gaa aga ctc aag aac ccc    1488
156 Gly Asp Val Gln Lys Leu Leu Ser Gly Glu Glu Arg Leu Lys Asn Pro
157             485             490             495
159 gac ctg att caa gta gga cac ttc tta ttc ggc ctc gct aac gag aag    1536
160 Asp Leu Ile Gln Val Gly His Phe Leu Phe Gly Leu Ala Asn Glu Lys
161             500             505             510
163 aga gcc aag gag ttg gag gcc act ttt ggc tgc cgg atg tca ccg gac    1584
164 Arg Ala Lys Glu Leu Glu Ala Thr Phe Gly Cys Arg Met Ser Pro Asp
165         515             520             525
167 atc aaa cag gaa ttg ctg caa tgc aaa gca cat ctt cat gca aat aag    1632
168 Ile Lys Gln Glu Leu Leu Gln Cys Lys Ala His Leu His Ala Asn Lys
169     530             535             540
172 ccc tta tcc gtg acc gac ctg aag gag gtc ttg ggc tgc ctg tat gag    1680
173 Pro Leu Ser Val Thr Asp Leu Lys Glu Val Leu Gly Cys Leu Tyr Glu
174 545             550             555             560
176 tct cag gag gag gag ctg gcg aag gtg gtg gtg gcc ccg ttc aag gaa    1728
177 Ser Gln Glu Glu Glu Leu Ala Lys Val Val Val Ala Pro Phe Lys Glu
178             565             570             575
180 att tct att cac ctg aca aat act tct gaa gtg atg cat tgt tcc ttc    1776
181 Ile Ser Ile His Leu Thr Asn Thr Ser Glu Val Met His Cys Ser Phe
182             580             585             590
184 agc ctg aag cat tgt caa gac ttg cag aaa ctc tca ctg cag gta gca    1824
185 Ser Leu Lys His Cys Gln Asp Leu Gln Lys Leu Ser Leu Gln Val Ala
186     595             600             605
188 aag ggg gtg ttc ctg gag aat tac atg gat ttt gaa ctg gac att gaa    1872
189 Lys Gly Val Phe Leu Glu Asn Tyr Met Asp Phe Glu Leu Asp Ile Glu
190     610             615             620
192 ttt gaa agc tca aac agc aac ctc aag ttt ctg gaa gtg aaa caa agc    1920
193 Phe Glu Ser Ser Asn Ser Asn Leu Lys Phe Leu Glu Val Lys Gln Ser
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194 625                   630                 635                   640
196 ttc ctg agt gac tct tct gtg cgg att ctt tgt gac cac gta acc cgt    1968
197 Phe Leu Ser Asp Ser Ser Val Arg Ile Leu Cys Asp His Val Thr Arg
198                   645                 650                   655
200 agc acc tgt cat ctg cag aaa gtg gag att aaa aac gtc acc cct gac    2016
201 Ser Thr Cys His Leu Gln Lys Val Glu Ile Lys Asn Val Thr Pro Asp
202                   660                 665                   670
204 acc gcg tac cgg gac ttc tgt ctt gct ttc att ggg aag aag acc ctc    2064
205 Thr Ala Tyr Arg Asp Phe Cys Leu Ala Phe Ile Gly Lys Lys Thr Leu
206             675                 680                 685
208 acg cac ctg acc ctg gca ggg cac atc gag tgg gaa cgc acg atg atg    2112
209 Thr His Leu Thr Leu Ala Gly His Ile Glu Trp Glu Arg Thr Met Met
210       690                 695                 700
212 ctg atg ctg tgt gac ctg ctc aga aat cat aaa tgc aac ctg cag tac    2160
213 Leu Met Leu Cys Asp Leu Leu Arg Asn His Lys Cys Asn Leu Gln Tyr
214 705                 710                 715                   720
216 ctg agg ttg gga ggt cac tgt gcc acc ccg gag cag tgg gct gaa ttc    2208
217 Leu Arg Leu Gly Gly His Cys Ala Thr Pro Glu Gln Trp Ala Glu Phe
218                   725                 730                 735
220 ttc tat gtc ctc aaa gcc aac cag tcc ctg aag cac ctg cgt ctc tca    2256
221 Phe Tyr Val Leu Lys Ala Asn Gln Ser Leu Lys His Leu Arg Leu Ser
222             740                 745                 750
224 gcc aat gtg ctc ctg gat gag ggt gcc atg ttg ctg tac aag acc atg    2304
225 Ala Asn Val Leu Leu Asp Glu Gly Ala Met Leu Leu Tyr Lys Thr Met
226             755                 760                 765
228 aca cgc cca aaa cac ttc ctg cag atg ttg tcg ttg gaa aac tgt cgt    2352
229 Thr Arg Pro Lys His Phe Leu Gln Met Leu Ser Leu Glu Asn Cys Arg
230       770                 775                 780
232 ctt aca gaa gcc agt tgc aag gac ctt gct gct gtc ttg gtt gtc agc    2400
233 Leu Thr Glu Ala Ser Cys Lys Asp Leu Ala Ala Val Leu Val Val Ser
234 785                 790                 795                   800
236 aag aag ctg aca cac ctg tgc ttg gcc aag aac ccc att ggg gat aca    2448
237 Lys Lys Leu Thr His Leu Cys Leu Ala Lys Asn Pro Ile Gly Asp Thr
238             805                 810                 815
240 ggg gtg aag ttt ctg t                                             2464
241 Gly Val Lys Phe Leu
242             820
244 <210> SEQ ID NO: 2
245 <211> LENGTH: 821
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 2
250 Met Thr Ser Pro Gln Leu Glu Trp Thr Leu Gln Thr Leu Leu Glu Gln
251 1               5                 10                  15
252 Leu Asn Glu Asp Glu Leu Lys Ser Phe Lys Ser Leu Leu Trp Ala Phe
253             20                  25                  30
254 Pro Leu Glu Asp Val Leu Gln Lys Thr Pro Trp Ser Glu Val Glu Glu
255         35                  40                  45
256 Ala Asp Gly Lys Lys Leu Ala Glu Ile Leu Val Asn Thr Ser Ser Glu
```

RAW SEQUENCE LISTING   DATE: 03/06/2002
PATENT APPLICATION: US/09/986,224   TIME: 12:40:28

Input Set : A:\07334-333001.txt
Output Set: N:\CRF3\03062002\I986224.raw

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257      50                  55                  60
258 Asn Trp Ile Arg Asn Ala Thr Val Asn Ile Leu Glu Glu Met Asn Leu
259 65                  70                  75                  80
260 Thr Glu Leu Cys Lys Met Ala Lys Ala Glu Met Met Glu Asp Gly Gln
261              85                  90                  95
262 Val Gln Glu Ile Asp Asn Pro Glu Leu Gly Asp Ala Glu Glu Asp Ser
263             100                 105                 110
264 Glu Leu Ala Lys Pro Gly Glu Lys Glu Gly Trp Arg Asn Ser Met Glu
265         115                 120                 125
266 Lys Gln Ser Leu Val Trp Lys Asn Thr Phe Trp Gln Gly Asp Ile Asp
267     130                 135                 140
268 Asn Phe His Asp Asp Val Thr Leu Arg Asn Gln Arg Phe Ile Pro Phe
269 145                 150                 155                 160
270 Leu Asn Pro Arg Thr Pro Arg Lys Leu Thr Pro Tyr Thr Val Val Leu
271                 165                 170                 175
272 His Gly Pro Ala Gly Val Gly Lys Thr Thr Leu Ala Lys Lys Cys Met
273             180                 185                 190
274 Leu Asp Trp Thr Asp Cys Asn Leu Ser Pro Thr Leu Arg Tyr Ala Phe
275         195                 200                 205
276 Tyr Leu Ser Cys Lys Glu Leu Ser Arg Met Gly Pro Cys Ser Phe Ala
277     210                 215                 220
278 Glu Leu Ile Ser Lys Asp Trp Pro Glu Leu Gln Asp Asp Ile Pro Ser
279 225                 230                 235                 240
280 Ile Leu Ala Gln Ala Gln Arg Ile Leu Phe Val Val Asp Gly Leu Asp
281             245                 250                 255
282 Glu Leu Lys Val Pro Pro Gly Ala Leu Ile Gln Asp Ile Cys Gly Asp
283             260                 265  ·                270
284 Trp Glu Lys Lys Lys Pro Val Pro Val Leu Leu Gly Ser Leu Leu Lys
285         275                 280                 285
286 Arg Lys Met Leu Pro Arg Ala Ala Leu Leu Val Thr Thr Arg Pro Arg
287     290                 295                 300
288 Ala Leu Arg Asp Leu Gln Leu Leu Ala Gln Gln Pro Ile Tyr Ile Arg
289 305                 310                 315                 320
290 Val Glu Gly Phe Leu Glu Glu Asp Arg Arg Ala Tyr Phe Leu Arg His
291                 325                 330                 335
292 Phe Gly Asp Glu Asp Gln Ala Met Arg Ala Phe Glu Leu Met Arg Ser
293             340                 345                 350
294 Asn Ala Ala Leu Phe Gln Leu Gly Ser Ala Pro Ala Val Cys Trp Ile
295         355                 360                 365
296 Val Cys Thr Thr Leu Lys Leu Gln Met Glu Lys Gly Glu Asp Pro Pro
297     370                 375                 380
298 Val Pro Ala Gly Arg Thr Ala Ala Gly Arg Ala Ala Asp Ala Glu Pro
299 385                 390                 395                 400
300 Pro Gly Arg Ala Gly Leu Trp Ala Gln Met Ser Val Phe His Arg Glu
301             405                 410                 415
302 Asp Leu Glu Arg Leu Gly Val Gln Glu Ser Asp Leu Arg Leu Phe Leu
303             420                 425                 430
304 Asp Gly Asp Ile Leu Arg Gln Asp Arg Val Ser Lys Gly Cys Tyr Ser
305         435                 440                 445
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VERIFICATION SUMMARY   DATE: 03/06/2002
PATENT APPLICATION: **US/09/986,224**   TIME: 12:40:29

Input Set : **A:\07334-333001.txt**
Output Set: **N:\CRF3\03062002\I986224.raw**

L:13 M:259 W: Allowed number of lines exceeded, <140> CURRENT APPLICATION NUMBER:
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date